



## UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE  
United States Patent and Trademark Office  
Address: COMMISSIONER OF PATENTS AND TRADEMARKS  
Washington, D.C. 20231  
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/508,997	06/27/2000	TOSHIO MIYATA	SHIM-004	5507

7590 09/25/2002  
KARL BOZICEVIC  
BOZICEVIC FIELD & FRANCIS  
200 MIDDLEFIELD ROAD  
SUITE 200  
MENLO PARK, CA 94025

EXAMINER

TURNER, SHARON L

ART UNIT PAPER NUMBER

1647

DATE MAILED: 09/25/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

RECEIVED

OCT 16 2002

TECH CENTER 1600/2900

DOCKETED

SEALIST 10/25/02  
LD 03/25/03



UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office  
COMMISSIONER OF PATENTS AND TRADEMARKS  
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Turner whose telephone number is (703) 308-0056. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Gary Kunz whose telephone number is (703) 308-4623. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

*Sharon Turner*  
9-23-02



**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached, to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**RECEIVED**

OCT 16 2002

TECH CENTER 1600/2900

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

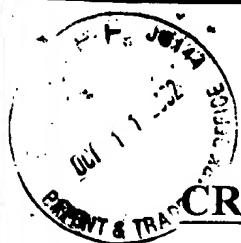
For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

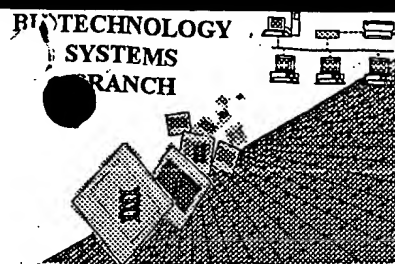
Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**



165



#8  
D3  
2/7/02  
1647

## CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/508,999  
Filing Date: 6/27/2001  
Date Processed by STIC: 1/26/2002

STIC Contact: Mark Spencer, 703-308-4212

RECEIVED

OCT 16 2002

TECH CENTER 1600/2900

RECEIVED  
FEB 05 2002  
TECH CENTER 1600/2900

### Nature of Problem:

The CRF (was):

- ☒ (circle one) Damaged or Unreadable (for Unreadable, see attached)  
☐ Blank (no files on CRF) (see attached)  
☐ Empty file (filename present, but no bytes in file) (see attached)  
☐ Virus-infected. Virus name: \_\_\_\_\_ The STIC will not process the CRF.  
☐ Not saved in ASCII text  
☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.  
☐ Did not contain a Sequence Listing. (see attached sample)  
☐ Other: \_\_\_\_\_

**PLEASE USE THE CHECKER VERSION 3.1 PROGRAM TO REDUCE ERRORS.  
SEE BELOW FOR ADDRESS:**

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel-Service , or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



## SEQUENCE LISTING

RECEIVED

OCT 16 2002

TECH CENTER 1600/2900

&lt;110&gt; MIYATA, Toshio

&lt;120&gt; Megsin Protein

&lt;130&gt; SHIM-004

&lt;140&gt; 09/508,997

&lt;141&gt; 2000-06-27

&lt;150&gt; JP 09-275302

&lt;151&gt; 1997-09-22

&lt;160&gt; 44

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1140)

&lt;400&gt; 1

atg gcc tcc ctt gct gca gca aat gca gag ttt tgc ttc aac ctg ttc 48

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe

1

5

10

15

aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct 96

Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20

25

30

ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat 144

Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp

35

40

45

gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca 192

Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser

50

55

60

gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg 240

Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu

65

70

75

80

aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc 288

Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu

85

90

95

agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag 336

Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys

100

105

110

gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga 384

Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg

115					120					125							
ggt	gac	ttt	acg	aat	cat	tta	gaa	gac	act	aga	cgt	aat	att	aat	aag	432	
Val	Asp	Phe	Thr	Asn	His	Leu	Glu	Asp	Thr	Arg	Arg	Asn	Ile	Asn	Lys		
130					135					140							
tgg	ggt	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aac	gtg	att	ggt	gaa	480	
Trp	Val	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Asn	Val	Ile	Gly	Glu		
145					150					155					160		
ggt	ggc	ata	agc	tca	tct	gct	gta	atg	gtg	ctg	gtg	aat	gct	gtg	tac	528	
Gly	Gly	Ile	Ser	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala	Val	Tyr		
165					170					175							
ttc	aaa	ggc	aag	tgg	caa	tca	gcc	ttc	acc	aag	agc	gaa	acc	ata	aat	576	
Phe	Lys	Gly	Lys	Trp	Gln	Ser	Ala	Phe	Thr	Lys	Ser	Glu	Thr	Ile	Asn		
180					185					190							
tgc	cat	ttc	aaa	tct	ccc	aag	tgc	tct	ggg	aag	gca	gtc	gcc	atg	atg	624	
Cys	His	Phe	Lys	Ser	Pro	Lys	Cys	Ser	Gly	Lys	Ala	Val	Ala	Met	Met		
195					200					205							
cat	cag	gaa	cgg	aag	ttc	aat	ttg	tct	ggt	att	gag	gac	cca	tca	atg	672	
His	Gln	Glu	Arg	Lys	Phe	Asn	Leu	Ser	Val	Ile	Glu	Asp	Pro	Ser	Met		
210					215					220							
aag	att	ctt	gag	ctc	aga	tac	aat	ggt	ggc	ata	aac	atg	tac	ggt	ctg	720	
Lys	Ile	Leu	Glu	Leu	Arg	Tyr	Asn	Gly	Gly	Ile	Asn	Met	Tyr	Val	Leu		
225					230					235					240		
ctg	cct	gag	aat	gac	ctc	tct	gaa	att	gaa	aac	aaa	ctg	acc	ttt	cag	768	
Leu	Pro	Glu	Asn	Asp	Leu	Ser	Glu	Ile	Glu	Asn	Lys	Leu	Thr	Phe	Gln		
245					250					255							
aat	cta	atg	gaa	tgg	acc	aat	cca	agg	cga	atg	acc	tct	aag	tat	ggt	816	
Asn	Leu	Met	Glu	Trp	Thr	Asn	Pro	Arg	Arg	Met	Thr	Ser	Lys	Tyr	Val		
260					265					270							
gag	gta	ttt	ttt	cct	cag	ttc	aag	ata	gag	aag	aat	tat	gaa	atg	aaa	864	
Glu	Val	Phe	Phe	Pro	Gln	Phe	Lys	Ile	Glu	Lys	Asn	Tyr	Glu	Met	Lys		
275					280					285							
caa	tat	ttg	aga	gcc	cta	ggg	ctg	aaa	gat	atc	ttt	gat	gaa	tcc	aaa	912	
Gln	Tyr	Leu	Arg	Ala	Leu	Gly	Leu	Lys	Asp	Ile	Phe	Asp	Glu	Ser	Lys		
290					295					300							
gca	gat	ctc	tct	ggg	att	gct	tcg	ggg	ggt	cgt	ctg	tat	ata	tca	agg	960	
Ala	Asp	Leu	Ser	Gly	Ile	Ala	Ser	Gly	Gly	Arg	Leu	Tyr	Ile	Ser	Arg		
305					310					315					320		
atg	atg	cac	aaa	tct	tac	ata	gag	gtc	act	gag	gag	ggc	acc	gag	gct	1008	
Met	Met	His	Lys	Ser	Tyr	Ile	Glu	Val	Thr	Glu	Glu	Gly	Thr	Glu	Ala		
325					330					335							
act	gct	gcc	aca	gga	agt	aat	att	gta	gaa	aag	caa	ctc	cct	cag	tcc	1056	
Thr	Ala	Ala	Thr	Gly	Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser		
340					345					350							

acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat 1104  
 Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp  
           355                                  360                                  365

gac atc atc tta ttc agt ggc aaa gtt tct tgc cct tga 1143  
 Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro  
           370                                  375                                  380

<210> 2  
 <211> 380  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe  
       1                                  5                                  10                                  15

Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser  
                   20                                  25                                  30

Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp  
           35                                  40                                  45

Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser  
       50                                  55                                  60

Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu  
       65                                  70                                  75                                  80

Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu  
                   85                                  90                                  95

Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys  
                   100                                  105                                  110

Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg  
           115                                  120                                  125

Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys  
       130                                  135                                  140

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu  
       145                                  150                                  155                                  160

Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
                   165                                  170                                  175

Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn  
                   180                                  185                                  190

Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met  
           195                                  200                                  205

His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met  
       210                                  215                                  220

Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu

225		230		235		240
Leu Pro Glu Asn Asp	Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln					
	245			250		255
Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val						
	260		265			270
Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys						
	275		280			285
Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys						
	290		295			300
Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg						
	305		310			315
Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala						
	325		330			335
Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser						
	340		345			350
Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp						
	355		360			365
Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro						
	370		375			380

<210> 3  
 <211> 1229  
 <212> DNA  
 <213> Rattus rattus

<220>  
 <221> CDS  
 <222> (8)..(1147)  
 <221> unsure  
 <222> (158)..(160), (287)..(289)  
 <223> n is unknown.

<400> 3		
tttcaaaa atg gcc tcc ctt gct gca gca aat gca gaa ttt ggc ttc gac		49
Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp		
1 5 10		
tta ttc aga gag atg gat agt agt caa gga aac gga aat gta ttc ttc		97
Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe		
15 20 25 30		
tct tcc ctg agc atc ttc act gcc ctg agc cta atc cgt ttg ggt gct		145
Ser Ser Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala		
35 40 45		
cga ggt gac tgt nnn cgt cag att gac aag gcc ctg cac ttt atc tcc		193
Arg Gly Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser		



50										55										60																			
cca	tca	aga	caa	ggg	aat	tca	tcg	aac	agt	cag	cta	gga	ctg	caa	tat	241																							
Pro	Ser	Arg	Gln	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Leu	Gly	Leu	Gln	Tyr																								
65										70										75																			
caa	ttg	aaa	aga	gtt	ctt	gct	gac	ata	aac	tca	tct	cat	aag	gat	nnn	289																							
Gln	Leu	Lys	Arg	Val	Leu	Ala	Asp	Ile	Asn	Ser	Ser	His	Lys	Asp	Xaa																								
80										85										90																			
aaa	ctc	agc	att	gcc	aat	gga	gtt	ttt	gca	gag	aaa	gta	ttt	gat	ttt	337																							
Lys	Leu	Ser	Ile	Ala	Asn	Gly	Val	Phe	Ala	Glu	Lys	Val	Phe	Asp	Phe																								
95										100										105										110									
cat	aag	agc	tat	atg	gag	tgt	gct	gaa	aac	tta	tac	aat	gct	aaa	gtg	385																							
His	Lys	Ser	Tyr	Met	Glu	Cys	Ala	Glu	Asn	Leu	Tyr	Asn	Ala	Lys	Val																								
115										120										125																			
gaa	aga	gtt	gat	ttt	aca	aat	gat	ata	caa	gaa	acc	aga	ttt	aaa	att	433																							
Glu	Arg	Val	Asp	Phe	Thr	Asn	Asp	Ile	Gln	Glu	Thr	Arg	Phe	Lys	Ile																								
130										135										140																			
aat	aaa	tgg	att	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aag	gtg	ttg	481																							
Asn	Lys	Trp	Ile	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Lys	Val	Leu																								
145										150										155																			
ggg	gac	agc	agc	ctc	agc	tca	tca	gct	gtc	atg	gtg	cta	gtg	aat	gct	529																							
Gly	Asp	Ser	Ser	Leu	Ser	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala																								
160										165										170																			
gtt	tac	ttc	aaa	ggc	aag	tgg	aaa	tcg	gcc	ttc	acc	aag	agt	gat	acc	577																							
Val	Tyr	Phe	Lys	Gly	Lys	Trp	Lys	Ser	Ala	Phe	Thr	Lys	Ser	Asp	Thr																								
175										180										185										190									
ctc	agt	tgc	cat	ttc	agg	tct	ccc	agc	ggt	cct	gga	aaa	gca	gtt	aat	625																							
Leu	Ser	Cys	His	Phe	Arg	Ser	Pro	Ser	Gly	Pro	Gly	Lys	Ala	Val	Asn																								
195										200										205																			
atg	atg	cat	caa	gaa	cgg	agg	ttc	aat	ttg	tct	acc	att	cag	gag	cca	673																							
Met	Met	His	Gln	Glu	Arg	Arg	Phe	Asn	Leu	Ser	Thr	Ile	Gln	Glu	Pro																								
210										215										220																			
cca	atg	cag	att	ctt	gag	cta	caa	tat	cat	ggt	ggc	ata	agc	atg	tac	721																							
Pro	Met	Gln	Ile	Leu	Glu	Leu	Gln	Tyr	His	Gly	Gly	Ile	Ser	Met	Tyr																								
225										230										235																			
atc	atg	ttg	ccc	gag	gat	gac	cta	tcc	gaa	att	gaa	agc	aag	ctg	agt	769																							
Ile	Met	Leu	Pro	Glu	Asp	Asp	Leu	Ser	Glu	Ile	Glu	Ser	Lys	Leu	Ser																								
240										245										250																			
ttc	cag	aat	cta	atg	gac	tgg	aca	aat	agc	agg	aag	atg	aaa	tct	cag	817																							
Phe	Gln	Asn	Leu	Met	Asp	Trp	Thr	Asn	Ser	Arg	Lys	Met	Lys	Ser	Gln																								
255										260										265										270									
tat	gtg	aat	gtg	ttt	ctc	ccc	cag	ttc	aag	ata	gag	aaa	gat	tat	gaa	865																							
Tyr	Val	Asn	Val	Phe	Leu	Pro	Gln	Phe	Lys	Ile	Glu	Lys	Asp	Tyr	Glu																								
275										280										285																			

atg agg agc cac ttg aaa tct gta ggc ttg gaa gac atc ttt gtt gag 913  
 Met Arg Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu  
 290 295 300

tcc agg gct gat ctg tct gga att gcc tct gga ggt cgt ctc tat gta 961  
 Ser Arg Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val  
 305 310 315

tca aag cta atg cac aag tcc ctc ata gag gtc tca gaa gaa ggc acc 1009  
 Ser Lys Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr  
 320 325 330

gag gca act gct gcc aca gaa agt aac atc gtt gaa aag cta ctt cct 1057  
 Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro  
 335 340 345 350

gaa tcc acg gtg ttc aga gct gac cgc ccc ttt ctg ttt gtc att agg 1105  
 Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg  
 355 360 365

aag aat ggc atc atc tta ttt act ggc aaa gtc tcg tgt cct 1147  
 Lys Asn Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro  
 370 375 380

tgaaattcta tttggttttc catacactaa caggcatgaa gaaacatcat aagtgaatag 1207  
 aattgtaatt ggaagtacat gg 1229

<210> 4  
 <211> 380  
 <212> PRT  
 <213> Rattus rattus  
  
 <220>  
 <221> UNSURE  
 <222> 51, 94  
 <223> Xaa is unknown.

<400> 4  
 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe  
 1 5 10 15

Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe Ser Ser  
 20 25 30

Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly  
 35 40 45

Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser  
 50 55 60

Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu  
 65 70 75 80

Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu  
 85 90 95

Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys  
 100 105 110  
 Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg  
 115 120 125  
 Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys  
 130 135 140  
 Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp  
 145 150 155 160  
 Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
 165 170 175  
 Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser  
 180 185 190  
 Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met  
 195 200 205  
 His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met  
 210 215 220  
 Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met  
 225 230 235 240  
 Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln  
 245 250 255  
 Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val  
 260 265 270  
 Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg  
 275 280 285  
 Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg  
 290 295 300  
 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys  
 305 310 315 320  
 Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala  
 325 330 335  
 Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser  
 340 345 350  
 Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn  
 355 360 365  
 Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro  
 370 375 380

<210> 5  
 <211> 1147  
 <212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1104)

<400> 5

ttc gac tta ttc aga gag atg gat agt agc caa gga aat gga aat gta	48
Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val	
1 5 10 15	
ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg	96
Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu	
20 25 30	
ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt	144
Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe	
35 40 45	
aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt	192
Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu	
50 55 60	
cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag	240
Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys	
65 70 75 80	
gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat	288
Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr	
85 90 95	
gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct	336
Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala	
100 105 110	
aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt	384
Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe	
115 120 125	
aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag	432
Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys	
130 135 140	
gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg	480
Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val	
145 150 155 160	
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act	528
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr	
165 170 175	
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta	576
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val	
180 185 190	
gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag	624
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln	
195 200 205	

cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc	672
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser	
210 215 220	
atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag	720
Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys	
225 230 235 240	
ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa	768
Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys	
245 250 255	
tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat	816
Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn	
260 265 270	
tat gaa atg acg cac cac ttg aaa tcc tta ggc ttg aaa gat atc ttt	864
Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe	
275 280 285	
gat gag tcc agt gca gat ctc tct gga att gcc tct gga ggt cgt ctc	912
Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu	
290 295 300	
tac gta tca aag cta atg cac aag tca ttc ata gag gtc tca gag gag	960
Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu	
305 310 315 320	
ggc act gaa gcc act gct gcc aca gaa aat aac att gtt gaa aag cag	1008
Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln	
325 330 335	
ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc	1056
Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val	
340 345 350	
atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct	1104
Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro	
355 360 365	
tgaaattcga tttggtttcc tatacagtaa caggcatcaa gaa	1147

<210> 6

<211> 368

<212> PRT

<213> Mus musculus

<400> 6

Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val
1 5 10 15

Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu
20 25 30

Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
35 40 45

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu  
 50 55 60  
 Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys  
 65 70 75 80  
 Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr  
 85 90 95  
 Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala  
 100 105 110  
 Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe  
 115 120 125  
 Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys  
 130 135 140  
 Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val  
 145 150 155 160  
 Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr  
 165 170 175  
 Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val  
 180 185 190  
 Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln  
 195 200 205  
 Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser  
 210 215 220  
 Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys  
 225 230 235 240  
 Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys  
 245 250 255  
 Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn  
 260 265 270  
 Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe  
 275 280 285  
 Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu  
 290 295 300  
 Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu  
 305 310 315 320  
 Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln  
 325 330 335  
 Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val  
 340 345 350  
 Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

<210> 7  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 7  
tgtaaaacga cggccagt 18

<210> 8  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 8  
accatgatta cgccaagctt g 21

<210> 9  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 9  
tcagagaggt cattc 15

<210> 10  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 10  
tcattgatgg gtcctcaa 18

<210> 11  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 11  
agattcttga gctcagat 18

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 12  
aatggtggca taaacatg 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 13  
acagacaaat tgaacttc 18

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 14  
gaattcatgg cctcccttgc tgcagcaaa 29

<210> 15  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 15  
gtcgacttat caagggcaag aaactttgcc 30

<210> 16  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence:synthesis

<400> 16

atgatctcag cattgtgaat g

21

<210> 17

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 17

actgagggag ttgcttttct ac

22

<210> 18

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 18

Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser	Thr	Leu	Phe	Arg
1				5				10					15	

<210> 19

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 19

Phe	Arg	Glu	Met	Asp	Asp	Asn	Gln	Gly	Asn	Gly	Asn	Val	Phe	Phe
1				5				10					15	

<210> 20

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 20

Ser	Gln	Ser	Gly	Leu	Gln	Ser	Gln	Leu	Lys	Arg	Val	Phe	Ser	Asp
1				5				10					15	

<210> 21

<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 21  
Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu  
1 5 10 15

<210> 22  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 22  
atcggatcca tggcctccct tgctgcagca aatgcaga 38

<210> 23  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 23  
ataagctttc atcaagggca agaaactttg cactgaata ag 42

<210> 24  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<221> misc feature  
<222> 26, 29  
<223> n is a or t or c or g.

<400> 24  
gtgaatgctg tgtacttaaa ggcaantgn 29

<210> 25  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<221> misc\_feature

<222> 3, 9, 15

<223> n is a or t or c or g.

<400> 25  
aanagraang grtcngc

17

<210> 26

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<221> misc\_feature

<222> 6, 9, 12, 15, 18, 21

<223> n is a or t or c or g.

<400> 26  
atggcntcng cngcngcngc naaygc

26

<210> 27

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 27  
cgacctccag aggcaattcc agagagatca gccctgg

37

<210> 28

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 28  
gtcttccaag cctacagatt tcaagtggct cctc

34

<210> 29

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 29  
gctcagggca gtgaagatgc tcaggaaga

30

<210> 30  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 30  
ctgacgtgca cagtcacctc gagcacc

27

<210> 31  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 31  
gaggtctcag aagaaggcac tgaggcaact gctgcc

36

<210> 32  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 32  
ctctatagga gacacttgg

19

<210> 33  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 33  
gaaacaaatc aaagcaaac

19

<210> 34  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 34  
gaaattgaaa rcaarctgas yttycagaat

30

<210> 35  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 35  
ctgasyttyc agaatactaat ggamtgac

29

<210> 36  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 36  
ggaytsaggr agtwgctttt cwacratrtt

30

<210> 37  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 37  
gaggtctcag aggagggcac tgaagccact gctgcc

36

<210> 38  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 38  
ccagtgcaga tctctctgga attgcctctg gaggtcgtc

39

<210> 39  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 39  
 gcctgttact gtataggaaa ccaaaccg 28  
  
 <210> 40  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 40  
 atggcytccc tygctgcwgc raatgcagar tttkgc 36  
  
 <210> 41  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 41  
 atcggatcca tggcctccct tgct 24  
  
 <210> 42  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 42  
 ataagctttc atcatcaagg gcaag 25  
  
 <210> 43  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 43  
 atggatccgc cgccatggcc tcccttgctg cagcaaatgc agag 44  
  
 <210> 44  
 <211> 27  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 44

tatcctgagg cagtgttaac aagcaac

27